

OIPE

RAW SEQUENCE LISTING

DATE: 02/06/2002

PATENT APPLICATION: US/10/054,295

TIME: 15:49:16

Input Set : N:\Crf3\RULE60\10054295.raw
Output Set: N:\CRF3\02062002\J054295.raw

## SEQUENCE LISTING

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3 (1) GENERAL INFORMATION:
      5
             (i) APPLICANT: Cech, Thomas R.
      6
                            Lingner, Joachim
      7
                                                             ENTERED
                            Nakamura, Toru
      8
                            Chapman, Karen B.
      9
                            Morin, Gregg B.
     10
                            Harley, Calvin
     11
                            Andrews, William H.
     13
            (ii) TITLE OF INVENTION: Novel Telomerase
     15
           (iii) NUMBER OF SEQUENCES: 225
     17
            (iv) CORRESPONDENCE ADDRESS:
                  (A) ADDRESSEE: Townsend and Townsend and Crew LLP
     18
     19
                  (B) STREET: Two Embarcadero Center, 8th Floor
     20
                  (C) CITY: San Francisco
     21
                  (D) STATE: California
                  (E) COUNTRY: United States of America
     22
                  (F) ZIP: 94111
     23
     25
             (V) COMPUTER READABLE FORM:
                  (A) MEDIUM TYPE: Floppy disk
     27
                  (B) COMPUTER: IBM PC compatible
                  (C) OPERATING SYSTEM: PC-DOS/MS-DOS
     28
     29
                  (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
     31
            (vi) CURRENT APPLICATION DATA:
C--> 32
                  (A) APPLICATION NUMBER: US/10/054,295
C--> 33
                  (B) FILING DATE: 18-Jan-2002
                  (C) CLASSIFICATION: 536
     51
           (vii) PRIOR APPLICATION DATA:
     37
                  (A) APPLICATION NUMBER: 08/854,050
     38
                  (B) FILING DATE:
     42
                  (A) APPLICATION NUMBER: US 08/846,017
     43
                  (B) FILING DATE: 25-APR-1997
     47
                  (A) APPLICATION NUMBER: US 08/844,419
     48
                  (B) FILING DATE: 18-APR-1997
     52
                  (A) APPLICATION NUMBER: US 08/724,643
     53
                  (B) FILING DATE: 01-OCT-1996
     56
          (viii) ATTORNEY/AGENT INFORMATION:
     57
                  (A) NAME: Apple, Randolph T.
     58
                  (B) REGISTRATION NUMBER: 36,429
     59
                  (C) REFERENCE/DOCKET NUMBER: 015389-002930US
     61
            (ix) TELECOMMUNICATION INFORMATION:
     62
                  (A) TELEPHONE: (415) 576-0200
     63
                  (B) TELEFAX: (415) 576-0300
```

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PATENT APPLICATION: US/10/054,295

65 (2) INFORMATION FOR SEQ ID NO: 1:												
67 (i) SEQUENCE CHARACTERISTICS:												
68 (A) LENGTH: 3279 base pairs												
69 (B) TYPE: nucleic acid	(B) TYPE: nucleic acid											
70 (C) STRANDEDNESS: single												
71 (D) TOPOLOGY: linear												
73 (ii) MOLECULE TYPE: other nucleic acid	,											
74 (A) DESCRIPTION: /desc = "DNA"												
76 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:												
78 AAAACCCCAA AACCCCAAAA CCCCTTTTAG AGCCCTGCAG TTGGAAATAT AACCTCAGTA	60											
80 TTAATAAGCT CAGATTTTAA ATATTAATTA CAAAACCTAA ATGGAGGTTG ATGTTGATAA	120											
82 TCAAGCTGAT AATCATGGCA TTCACTCAGC TCTTAAGACT TGTGAAGAAA TTAAAGAAGC	180											
84 TAAAACGTTG TACTCTTGGA TCCAGAAAGT TATTAGATGA AGAAATCAAT CTCAAAGTCA	240											
86 TTATAAAGAT TTAGAAGATA TTAAAATATT TGCGCAGACA AATATTGTTG CTACTCCACG	300											
88 AGACTATAAT GAAGAAGATT TTAAAGTTAT TGCAAGAAAA GAAGTATTTT CAACTGGACT	360											
90 AATGATCGAA CTTATTGACA AATGCTTAGT TGAACTTCTT TCATCAAGCG ATGTTTCAGA	420											
92 TAGACAAAAA CTTCAATGAT TTGGATTTCA ACTTAAGGGA AATCAATTAG CAAAGACCCA	480											
94 TTTATTAACA GCTCTTTCAA CTCAAAAGCA GTATTTCTTT CAAGACGAAT GGAACCAAGT	540											
96 TAGAGCAATG ATTGGAAATG AGCTCTTCCG ACATCTCTAC ACTAAATATT TAATATTCCA	600											
98 GCGAACTTCT GAAGGAACTC TTGTTCAATT TTGCGGGAAT AACGTTTTTG ATCATTTGAA	660 .											
100 AGTCAACGAT AAGTTTGACA AAAAGCAAAA AGGTGGAGCA GCAGACATGA ATGAACCTCG	720											
102 ATGTTGATCA ACCTGCAAAT ACAATGTCAA GAATGAGAAA GATCACTTTC TCAACAACAT	780											
104 CAACGTGCCG AATTGGAATA ATATGAAATC AAGAACCAGA ATATTTTATT GCACTCATTT	840											
106 TAATAGAAAT AACCAATTCT TCAAAAAGCA TGAGTTTGTG AGTAACAAAA ACAATATTTC	900											
108 AGCGATGGAC AGAGCTCAGA CGATATTCAC GAATATATTC AGATTTAATA GAATTAGAAA	960											
110 GAAGCTAAAA GATAAGGTTA TCGAAAAAAT TGCCTACATG CTTGAGAAAG TCAAAGATTT	1020											
112 TAACTTCAAC TACTATTTAA CAAAATCTTG TCCTCTTCCA GAAAATTGGC GGGAACGGAA	1080											
114 ACAAAAAATC GAAAACTTGA TAAATAAAAC TAGAGAAGAA AAGTCGAAGT ACTATGAAGA	1140											
116 GCTGTTTAGC TACACAACTG ATAATAAATG CGTCACACAA TTTATTAATG AATTTTTCTA	1200											
118 CAATATACTC CCCAAAGACT TTTTGACTGG AAGAAACCGT AAGAATTTTC AAAAGAAAGT	1260											
120 TAAGAAATAT GTGGAACTAA ACAAGCATGA ACTCATTCAC AAAAACTTAT TGCTTGAGAA	1320											
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126 CGTCGTCTCG CTGATTAGAT GATTTTTCTA TGTCACCGAG CAACAGAAAA GTTACTCCAA	1500											
128 AACCTATTAC TACAGAAAGA ATATTTGGGA CGTCATTATG AAAATGTCAA TCGCAGACTT	1560											
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134 GACTTTCAAT AAGAAGATTG TAAATTCAGA CCGGAAGACT ACAAAATTAA CTACAAATAC	1740											
136 GAAGTTATTG AACTCTCACT TAATGCTTAA GACATTGAAG AATAGAATGT TTAAAGATCC	1800											
138 TTTTGGATTC GCTGTTTTTA ACTATGATGA TGTAATGAAA AAGTATGAGG AGTTTGTTT	1860											
140 CAAATGGAAG CAAGTTGGAC AACCAAAACT CTTCTTTGCA ACTATGGATA TCGAAAAGTG	1920											
142 ATATGATAGT GTAAACAGAG AAAAACTATC AACATTCCTA AAAACTACTA AATTACTTTC												
144 TTCAGATTTC TGGATTATGA CTGCACAAAT TCTAAAGAGA AAGAATAACA TAGTTATCGA												
146 TTCGAAAAC TTTAGAAAGA AAGAAATGAA AGATTATTTT AGACAGAAAT TCCAGAAGAT												
148 TGCACTTGAA GGAGGACAAT ATCCAACCTT ATTCAGTGTT CTTGAAAATG AACAAAATGA												
150 CTTAAATGCA AAGAAAACAT TAATTGTTGA AGCAAAGCAA												
152 TAACTTACTT CAACCAGTCA TTAATATTTG CCAATATAAT TACATTAACT TTAATGGGAA												
154 GTTTTATAAA CAAACAAAAG GAATTCCTCA AGGTCTTTGA GTTTCATCAA TTTTGTCATC												
156 ATTTTATTAT GCAACATTAG AGGAAAGCTC CTTAGGATTC CTTAGAGATG AATCAATGAA												

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158 CCCTGAAAAT CCAAATGTTA ATCTTCTAAT GAGACTTACA GATGACTATC TTTTGATTAC
                                                                                2460
     160 AACTCAAGAG AATAATGCAG TATTGTTTAT TGAGAAACTT ATAAACGTAA GTCGTGAAAA
                                                                                2520
     162 TGGATTTAAA TTCAATATGA AGAAACTACA GACTAGTTTT CCATTAAGTC CAAGCAAATT
                                                                                2580
     164 TGCAAAATAC GGAATGGATA GTGTTGAGGA GCAAAATATT GTTCAAGATT ACTGCGATTG
                                                                                2640
     166 GATTGGCATC TCAATTGATA TGAAAACTCT TGCTTTAATG CCAAATATTA ACTTGAGAAT
                                                                                2700
     168 AGAAGGAATT CTGTGTACAC TCAATCTAAA CATGCAAACA AAGAAAGCAT CAATGTGGCT
                                                                                2760
     170 CAAGAAGAA CTAAAGTCGT TTTTAATGAA TAACATTACC CATTATTTTA GAAAGACGAT
                                                                                2820
     172 TACAACCGAA GACTTTGCGA ATAAAACTCT CAACAAGTTA TTTATATCAG GCGGTTACAA
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    174 ATACATGCAA TGAGCCAAAG AATACAAGGA CCACTTTAAG AAGAACTTAG CTATGAGCAG
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     176 TATGATCGAC TTAGAGGTAT CTAAAATTAT ATACTCTGTA ACCAGAGCAT TCTTTAAATA
    178 CCTTGTGTGC AATATTAAGG ATACAATTTT TGGAGAGGAG CATTATCCAG ACTTTTTCCT
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    180 TAGCACACTG AAGCACTTTA TTGAAATATT CAGCACAAAA AAGTACATTT TCAACAGAGT
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    182 TTGCATGATC CTCAAGGCAA AAGAAGCAAA GCTAAAAAGT GACCAATGTC AATCTCTAAT
    184 TCAATATGAT GCATAGTCGA CTATTCTAAC TTATTTTGGA AAGTTAATTT TCAATTTTTG
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    186 TCTTATATAC TGGGGTTTTG GGGTTTTGGG GTTTTGGGG
                                                                                3279
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              (i) SEQUENCE CHARACTERISTICS:
                   (A) LENGTH: 1031 amino acids
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    192
                   (B) TYPE: amino acid
     193
                   (C) STRANDEDNESS: Not Relevant
W--> 194
                   (D) TOPOLOGY: Not Relevant
             (ii) MOLECULE TYPE: protein
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    198
             (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
     200
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    201
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    204
    206
              Trp Ile Gln Lys Val Ile Arg Cys Arg Asn Gln Ser Gln Ser His Tyr
    207
                                           40
    209
              Lys Asp Leu Glu Asp Ile Lys Ile Phe Ala Gln Thr Asn Ile Val Ala
    210
                                       55
              Thr Pro Arg Asp Tyr Asn Glu Glu Asp Phe Lys Val Ile Ala Arg Lys
    212
    213
                                  70
                                                       75
    215
              Glu Val Phe Ser Thr Gly Leu Met Ile Glu Leu Ile Asp Lys Cys Leu
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    221
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                                                               125
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                                       135
    227
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    230
              Thr Lys Tyr Leu Ile Phe Gln Arg Thr Ser Glu Gly Thr Leu Val Gln
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                                                   170
    233
              Phe Cys Gly Asn Asn Val Phe Asp His Leu Lys Val Asn Asp Lys Phe
    234
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    236
              Asp Lys Lys Gln Lys Gly Gly Ala Ala Asp Met Asn Glu Pro Arg Cys
    237
                      195
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239 240	Cys	Ser 210	Thr	Cys	Lys	Tyr	Asn 215	Va1	Lys ·	Asn	Glu	Lys 220	Asp	His	Phe	Leu
242	Asn		Ile	Asn	Val	Pro		Trp	Asn	Asn	Met		Ser	Arg	Thr	Arg
243	225					230					235					240
245	Ile	Phe	Tyr	Cys	Thr	His	Phe	Asn	Arg	Asn	Asn	Gln	Phe	Phe	Lys	Lys
246					245					250					255	
248	His	Glu	Phe		Ser	Asn	Lys	Asn		Ile	Ser	Ala	Met	_	Arg	Ala
249			<b>-</b>	260					265					270	_	
251	Gln	Thr	Ile	Phe	Thr	Asn	Ile		Arg	Phe	Asn	Arg		Arg	Lys	Lys
252	T	· • •	275	T	17- 7	т1.	<b>a</b> 1	280	<b>~</b> 1.	21-	m	16-A	285	<b>a</b> 1	T	17- 1
254 255	Leu	290	Asp	гаг	vai	TTE	295	ьуѕ	TTE	Ата	TAT	300	ьеи	GIU	ьуѕ	Val
257	Luc		Phe	Δen	Dho	Δen	_	Tur	T.011	Thr	Lve		Cvc	Pro	Leu	Pro
258 ·	305	пор	1 110	non	1 110	310	- Y -	111	ВСα	TILL	315	JCI	Cys	110	пси	320
260		Asn	Trp	Ara	Glu		Lvs	Gln	Lvs	Ile		Asn	Leu	Ile	Asn	-
261				5	325	5	-1-		-1-	330					335	-1-
263	Thr	Arg	Glu	Glu	Lys	Ser	Lys	Tyr	Tyr	Glu	Glu	Leu	Phe	Ser	Tyr	Thr
264			•	340	_			_	345					350	_	
266	Thr	Asp	Asn	Lys	Cys	Val	Thr	Gln	Phe	Ile	Asn	Glu	Phe	Phe	Tyr	Asn
267			355					360					365			
269	Ile	Leu	Pro	Lys	Asp	Phe	Leu	Thr	Gly	Arg	Asn	Arg	Lys	Asn	Phe	Gln
270		370					375					380				
272	_	Lys	Val	Lys	Lys	_	Val	Glu	Leu	Asn	_		Glụ	Leu	Ile	
273	385	_		_	_	390	_	1	_	1	395.		~ 1	_	_	400
275	ьys	Asn	Leu	Leu		GIU	ьуs	тте	Asn		Arg	GIU	тте	ser	_	мет
276	Cln	170.7	Glu	mb m	405	7 J -	T	ni a	Dho	410	m	Dho	7 00	ni a	415	N a n
278 279	GIII	val	GIU	420	ser	Ата	гÀг	нтэ	425	тут	тут	Pne	ASP	430	GIU	ASII
281	Tlo	Фυν	Val		Trn	T.vc	T.OII	T.611		Tra	τlΔ	Dhe	Glu		Len	Va 1
282	110	- y -	435		111	цуз	пец	440	mrg	111	110	1110	445	пор	шса	VUI
284		Ser	Leu		Ara	Cvs	Phe		Tvr	Val	Thr	Glu		Gln	Lvs	Ser
285	,	450			5	-1-	455		- 4 -	,		460			-1-	
287	Tyr	Ser	Lys	Thr	Tyr	Tyr	Tyr	Arg	Lys	Asn	Ile	Trp	Asp	Val	Ile	Met
288.	465		_		_	470	_	_	_		475	_	_			480
290	Lys	Met	Ser	Ile	Ala	Asp	Leu	Lys	Lys	Glu	Thr	Leu	Ala	Glu	Val	Gln
291					485					490					495	
293	Ģlu	Lys	Glu		Glu	Glu	$\mathtt{Trp}$	Lys	_	Ser	Leu	Gly	Phe		Pro	Gly
294				500					505	_				510		_
296	Lys	Leu	Arg		Ile	Pro	Lys	_	Thr	Thr	Phe	Arg		Ile	Met	Thr
297	_1	_	515			1	_	520	_	_	_	_,	525	_	_	m1
299	Phe		Lys	Lys	11e	Val		ser	Asp	Arg	Lys		Thr	Lys	Leu	Thr
300		530	mh	T	т он	т о	535	002	TI d	T au	Wot	540	T	шь»	T 011	T 110
302 303	545	ASII	Thr	пλг	ьeu	550	ASII	261	птз	ьеи	мес 555	пец	пуз	TIII	ьeu	560
305		Δτα	Met	Dho	Lve		Pro	Dho	G1v	Dha		Va 1	Dh≏	Δen	ጥህድ	
306	กอแ	AT 9	Met	1116	565	42h	110	r ne	G T Y	570	лта	v a I	F 116	พวแ	575	-12P
308	Asp	Va1	Met	Lvs		Tvr	Glu	Glu	Phe		Cvs	Lvs	Tro	Lvs		Val
309	[			580	-1-	- <b></b>			585		-1-	-1-	F	590		
311	Gly	Gln	Pro		Leu	Phe	Phe	Ala		Met	Asp	Ile	Glu		Cys	Tyr
	_			_							-					

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Asp   Ser. Val   Asn   Asp   Glu   Lys   Leu   Ser   Thr   Phe   Leu   Lys   Thr   Thr   Lys   Glo	212			595					600					605			
115	312	7 ~			7	7 ~~~	C1	Tura			mh∽	Dho	Т оп		mb ~	mh∽	T
Leu Leu Ser Ser Asp Phe Trp I le Met Thr Ala GIn I le Leu Lys Arg 625		AS		· vaı	ASI	Arg	GIU	_	ьeu	ser	THE	Pne		гуѕ	THE	THE	гуѕ
118		_		_	_	_	<b>51</b>		<b>1</b>		-1			1	-	-	
192   193   194   195   196   195   196   195   196   195   196   195   196   195   196   195   196   195   196   195   196   195   196   195   196   195   196   195   196   195   196   195   196   195   196   195   196   195   196   195   195   196   195				Ser	Ser	Asp		Trp	тте	Met	Thr		GIn	тте	Leu	ьуs	-
121																	
1923   Lys   Asp   Tyr   Phe   Arg   Gln   Lys   Phe   Gln   Lys   Ile   Ala   Leu   Glu   Gly   Gly   G66   G66   G66   G66   G70   G70		Lys	s Asn	Asn	Ile		Ile	Asp	Ser	Lys		Phe	Arg	Lys	Lys		Met
326								7	:								
Second	323	Lys	3 Asp	Tyr		Arg	Gln	Lys	Phe		Lys	Ile	Ala	Leu	Glu	Gly	Gly
327	324			•	66.0					665	•				670		
329	326	Gli	ı Tyr	Pro	Thr	Leu	Phe	Ser	Val	Leu	Glu	Asn	Glu	Gln	Asn	Asp	Leu
330	327			675					680					685			
332	329	Ası	ı Ala	Lys	Lys	Thr	Leu	Ile	Val	Glu	Ala	Lys	Gln	Arg	Asn	Tyr	Phe
333	330		690					695					700				
Tyr   Tile   Asn   Phe   Asn   Gly   Lys   Phe   Tyr   Lys   Gln   Thr   Lys   Gly   Tile   Pro   735	332	Lys	Lys	Asp	Asn	Leu	Leu	Gln	Pro	Val	Ile	Asn	Ile	Cys	Gln	Tyr	Asn
336	333	705	<b>j</b>	•			710					715					720
338         Gln         Gly         Leu         Cys         Val         Ser         Jee         Jee         Ser         Jee         Jee         Reg         Pro         Ala         Thr         Ala         Thr         Ala         Thr         Ala         Thr         Ala         Thr         Ala         Pro         Asn         Leu         Leu         Leu         Arg         Asp         Glu         Ser         Me         Asn         Leu         Arg         Arg         Leu         Thr         Asp         Asp         Val         Asp         Leu         Leu         Pro         Asp         Arg         Arg         Leu         Thr         Asp         Arg         Arg         Leu         Thr         Asp         Arg         Arg         Leu         Thr         Asp         Arg         Leu         Arg         Arg         Leu         Arg         Brb         Arg	335	Туз	lle	Asn	Phe	Asn	Gly	Lys	Phe	Tyr	Lys	Gln	Thr	Lys	Gly	Ile	Pro
339         Leu         Glu         Ser         Ser         Leu         Gly         Phe         Leu         Arg         Asp         Glu         Ser         Met         Asn         Pro           342         755         75         57         Ser         Leu         Gly         Phe         Leu         Arg         Asp         Glu         Ser         Met         Asn         Pro         760         760         765         765         765         746         765         746         765         746         765         746         765         746         765         746         765         746         765         746         746         765         746         740         780         780         780         740         780	336					725					730		,			735	
339         Leu         Glu         Ser         Ser         Leu         Gly         Phe         Leu         Arg         Asp         Glu         Ser         Met         Asn         Pro           342         755         755         For         Leu         Gly         Phe         Leu         Arg         Asp         Glu         Ser         Met         Asn         Pro         760         760         765         765         765         746         765         746         765         746         765         765         746         765         746         765         746         765         746         765         746         765         746         746         760         760         780	338	Glr	Gly	Leu	Cys	Val	Ser	Ser	·Ile	Leu	Ser	Ser	Phe	Tyr	Tyr	Ala	Thr
342       Glu       Asn       Pro       Asn       Val       Asn       Leu       Leu       Leu       Arg       Leu       Th       Asp       Asp       Tyr       Leu         345       770       770       770       770       775       780       780       780       1       Leu       Asp       Asp       Asp       Tyr       Leu       Asp       Tyr       Gu       Asp       Leu       Asp       Asp </td <td>339</td> <td></td> <td>_</td> <td></td> <td>740</td> <td></td> <td></td> <td></td> <td></td> <td>745</td> <td></td> <td></td> <td></td> <td>_</td> <td>750</td> <td></td> <td></td>	339		_		740					745				_	750		
342       Glu       Asn       Pro       Asn       Val       Asn       Leu       Leu       Leu       Arg       Leu       Th       Asp       Asp       Tyr       Leu         345       770       770       770       770       775       780       780       780       1       Leu       Asp       Asp       Asp       Tyr       Leu       Asp       Tyr       Gu       Asp       Leu       Asp       Asp </td <td>341</td> <td>Lei</td> <td>Glu</td> <td>Glu</td> <td>Ser</td> <td>Ser</td> <td>Leu</td> <td>Gly</td> <td>Phe</td> <td>Leu</td> <td>Arq</td> <td>Asp</td> <td>Glu</td> <td>Ser</td> <td>Met</td> <td>Asn</td> <td>Pro</td>	341	Lei	Glu	Glu	Ser	Ser	Leu	Gly	Phe	Leu	Arq	Asp	Glu	Ser	Met	Asn	Pro
345       770       775       775       780         347       Leu Ile Thr Thr Thr Gln Glu Asn Asn Ala Val Leu Phe Ile Glu Lys Roo       795       800         350       Ile Asn Val Ser Arg Glu Asn Gly Phe Lys Phe Asn Met Lys Lys Leu 805       815       815         351       Gln Thr Ser Phe Pro Leu Ser Pro Ser Lys Phe Asn Met Lys Tyr Gly Met 825       815       815         353       Gln Thr Ser Phe Pro Leu Ser Pro Ser Lys Phe Asn Met Lys Tyr Gly Met 825       820       825       825       830         356       Asp Ser Val Glu Glu Glu Gln Asn B40       810       845       835       840       845         357       835       850       835       840       845       845         360       850       850       850       860       860         362       Leu Arg Ile Glu Gly Ile Leu Cys Thr Leu Asn Leu Asn Met Gln Thr 863       865       860       860         365       Lys Lys Ala Ser Met Trp Leu Cys Thr Leu Asn Leu Asn Leu Asn Met Gln Thr 863       865       870 <td>342</td> <td></td> <td></td> <td>755</td> <td></td> <td></td> <td></td> <td>_</td> <td>760</td> <td></td> <td>_</td> <td>_</td> <td></td> <td>765</td> <td></td> <td></td> <td>•</td>	342			755				_	760		_	_		765			•
345       Leu       Ile       Thr       Thr       Gln       Asn       Asn       Ala       Val       Leu       Phe       Ile       Glu       Lys       Leu         347       Leu       Ile       Thr       Thr       Glu       Asn       Asn       Ala       Val       Leu       Phe       Ros       Tys       Lys       L	344	Glı	Asn	Pro	Asn	Val	Asn	Leu	Leu	Met	Arq	Leu	Thr	Asp	Asp	Tyr	Leu
348       785	345										_			-	-	-	
348       785	347	Leu	Ile	Thr	Thr	Gln	Glu	Asn	Asn	Ala	Val	Leu	Phe	Ile	Glu	Lys	Leu
Solution   Solution	348														-	-	
351       Gln       Thr       Ser       Phe Phe Phe Pro Leu Ser       Pro Ser Pro Ser Pro Ser Lys       Lys       Phe Ala Lys       Tyr       Gly Met Ser Gly         354       Asp       Ser Val Glu Glu Glu Glu Glu Glu Glu Glu Glu Gl	350	Ile	Asn	Val	Ser	Arq	Glu	Asn	Gly	Phe	Lys	Phe	Asn	Met	Lys	Lys	Leu
353         Gln         Thr         Ser         Phe         Pro         Leu         Ser         Lys         Phe         Ala         Lys         Tyr         Gly         Met         Asp         Ser         Val         Glu         Glu         Glu         Asp         Ile         Val         Glu         Asp         Ile         Val         Glu         Asp         Met         Lys         Bato         Ile         Asp         Tyr         Cys         Asp         Tyr         Lys         Asp         Tyr         Lys         Asp         Lys         Tyr         Lys         Lys         Lys         Lys         Lys         Lys         Lys         Asp         Ile         Asp         Met         Lys         Tyr         Lys         Lys <td>351</td> <td></td> <td></td> <td></td> <td></td> <td>_</td> <td></td> <td></td> <td>-</td> <td></td> <td>_</td> <td></td> <td></td> <td></td> <td>-</td> <td>_</td> <td></td>	351					_			-		_				-	_	
354       820       825       830       830         356       Asp       Ser       Val       Glu       Glu       Gln       Asp       Tyr       Cys       Asp       Trp       Ile         357       835       835       840       840       855       845       845       855       860       850       850       850       855       860       8		Glr	Thr	Ser	Phe	Pro	Leu	Ser	Pro	Ser	Lvs	Phe	Ala	Lvs	Tvr	Glv	Met
356       Asp Ser Val Glu Glu Glu Glu Glu Glu Asp Str Bash Registration       Asp Ser Val Glu Glu Glu Glu Glu Glu Glu Glu Glu Gl											_1 -			-1-	_	- 1	
357       835       840       845       8		Asr	Ser	Val		Glu	Gln	Asn	Ile	Val	Gln	Asp	Tvr	Cvs	Asp	Trp	Ile
359 Gly Ile Ser Ile Asp Met Lys Thr Leu Ala Leu Met Pro Asn Ile Asn 360 850 850 850 855 860 860 860 860 860 860 860 860 860 860														_			
360       850       855       860         362       Leu Arg       Ile Glu Gly       Ile Leu Cys Thr Leu Asn Leu Asn Met Gln Thr         363       865       865       870       875       875       880         365       Lys Lys Ala Ser Met Trp Leu Lys Lys Lys Lys Beu Phe Ben Ser Ser Phe Leu Met Ser Ser Ser Met His Tyr Phe Arg Lys Thr Ile Thr Thr Glu Asp Phe Ser Ser Ser Ser Met Ile Asp Leu Phe Ile Ser Gly Gly Tyr Lys Tyr Ser Ser Ser Met Ile Asp Leu Glu Val Ser His Phe Lys Lys Asn Leu Ala Ser Ser Ser Met Ile Asp Leu Glu Val Ser Lys Ile Ile Tyr Ser Val Ser Ser Ser Met Ile Ser Ser Thr Leu Val Cys Asn Ile Lys Asp Thr Ile Ser Ser Ser Met Ile Ser Ser Val Ser Ser Ser Ser Met Ile Ser Ser Ser Ser Ser Ser Ser Ser Ser Se		Glv	Ile		Ile	Asp	Met	Lvs		Leu	Ala	Leu	Met	Pro	Asn	Ile	Asn
362       Leu Arg 1le Glu Gly Ile Glu Cys Thr Leu Asn Leu Asn Met Gln Thr 863       865								_									
363       865       870       875       880         365       Lys       Lys       Ala       Ser       Met       Trp       Leu       Lys       Lys       Leu       Lys       Ser       Phe       Leu       Met         366       Asn       Asn       Ile       Thr       His       Tyr       Phe       Arg       Lys       Thr       Ile       Thr       Glu       Asp       Phe         369       Breek       Asn       Asn       Ile       Thr       His       Tyr       Phe       Arg       Lys       Thr       Ile       Thr       Glu       Asp       Phe       Phe       Ile       Thr       Ile       Thr       Glu       Asp       Phe       Ile       Ser       Gly       Gly       Tyr       Lys       Asp       His       Phe       Ile       Ser       Gly       Tyr       Lys       Tyr       Phe       Ile       Ile       Ile       Ile       Ile       Asp       Ile       Asp       Ile       Ile       Ile       Asp       Ile       Asp       Ile       Ile <td< td=""><td></td><td>Leu</td><td></td><td>Ile</td><td>Glu</td><td>Glv</td><td>Ile</td><td>-</td><td>Cvs</td><td>Thr</td><td>Leu</td><td>Asn</td><td></td><td>Asn</td><td>Met</td><td>Gln</td><td>Thr</td></td<>		Leu		Ile	Glu	Glv	Ile	-	Cvs	Thr	Leu	Asn		Asn	Met	Gln	Thr
365       Lys       Lys       Ala       Ser       Met       Trp       Leu       Lys       Lys       Leu       Lys       Ser       Phe       Leu       Met         366       Asn       Asn       Ile       Thr       His       Tyr       Phe       Arg       Lys       Thr       Ile       Thr       Glu       Asp       Phe         369       Asn       Asn       Asn       Ile       Thr       His       Tyr       Phe       Arg       Lys       Thr       Ile       Thr       Glu       Asp       Phe       Phe       Arg       Lys       Thr       Ile       Thr       Glu       Asp       Phe       Ile       Ser       Gly       Gly       Tyr       Lys       Tyr       Ile       Ser       Gly       Tyr       Lys       Tyr       Ile       I						1			-1-								
366       Asn Asn Ile Thr His Tyr Phe Arg Lys Thr Ile Thr Thr Glu Asp Phe         368       Asn Asn Ile Thr His Tyr Phe Arg Lys Thr Ile Thr Thr Glu Asp Phe         369       900       900       905       905       910       910         371       Ala Asn Lys Thr Leu Asn Lys Leu Phe Ile Ser Gly Gly Tyr Lys Tyr 925       925       925       925         374       Met Gln Cys Ala Lys Glu Tyr Lys Asp His Phe Lys Lys Lys Asn Leu Ala 930       930       935       940       940       940         377       Met Ser Ser Met Ile Asp Leu Glu Val Ser Lys Ile Ile Tyr Ser Val 945       950       955       960         380       Thr Arg Ala Phe Phe Lys Tyr Leu Val Cys Asn Ile Lys Asp Thr Ile 970       975         381       Phe Gly Glu Glu His Tyr Pro Asp Phe Phe Leu Ser Thr Leu Lys His				Ala	Ser	Met.		Leu	Lvs	Lvs	Lvs		Lvs	Ser	Phe	Leu	
368       Asn Asn Ile Thr His Tyr Phe Arg Lys Thr Ile Thr Thr Glu Asp Phe         369       900       900       905       11e Thr Thr Glu Asp Phe       910         371       Ala Asn Lys Thr Leu Asn Lys Leu Phe Ile Ser Gly Gly Tyr Lys Tyr 925       77       915       920       920       925       925         374       Met Gln Cys Ala Lys Glu Tyr Lys Asp His Phe Lys Lys Lys Asn Leu Ala 930       930       935       940       940       11e Tyr Ser Val 940         377       Met Ser Ser Ser Met Jle Asp Leu Glu Val Ser Lys Jle Ile Tyr Ser Val 940       950       955       960         380       Thr Arg Ala Phe Phe Lys Tyr Leu Val Cys Asn Ile Lys Asp Thr Ile 970       975         381       Phe Gly Glu Glu Glu His Tyr Pro Asp Phe Phe Leu Ser Thr Leu Lys His		-1-	-1-						-1-	-1-	_		-1-				
369 371 Ala Asn Lys Thr Leu Asn Lys Leu Phe Ile Ser Gly Gly Tyr Lys Tyr 915 372 374 Met Gln Cys Ala Lys Glu Tyr Lys Asp His Phe Lys Lys Asn Leu Ala 930 375 Met Ser Ser Met Ile Asp Leu Glu Val Ser Lys Ile Ile Tyr Ser Val 940 377 Met Ser Ser Met Ile Asp Leu Glu Val Ser Lys Ile Ile Tyr Ser Val 950 380 Thr Arg Ala Phe Phe Lys Tyr Leu Val Cys Asn Ile Lys Asp Thr Ile 965 381 Phe Gly Glu Glu His Tyr Pro Asp Phe Phe Leu Ser Thr Leu Lys His		Asr	Asn	Ile	Thr		Tvr	Phe	Ara	Lvs		Tle	Thr	Thr	Glu		Phe
371 Ala Asn Lys Thr Leu Asn Lys Leu Phe Ile Ser Gly Gly Tyr Lys Tyr 372  374 Met Gln Cys Ala Lys Glu Tyr Lys Asp His Phe Lys Lys Asn Leu Ala 930  375 930							-1-		• 9	_							
372 915 920 925 925 925 926 374 Met Gln Cys Ala Lys Glu Tyr Lys Asp His Phe Lys Lys Asn Leu Ala 375 930 930 935 940 940 935 940 940 957 940 957 960 955 960 960 960 960 965 965 965 965 965 965 965 965 965 965		Ala	Asn	Lvs		Len	Asn	Lvs	Len		Tle	Ser	Glv	Glv		Lvs	Tvr
374 Met Gln Cys Ala Lys Glu Tyr Lys Asp His Phe Lys Lys Asn Leu Ala 375 930		1110				Lou		_10		1 110	110	001	0-1		-1-	2,0	-1-
375 930 935 935 940  377 Met Ser Ser Met Ile Asp Leu Glu Val Ser Lys Ile Ile Tyr Ser Val  378 945 950 950 955 960  380 Thr Arg Ala Phe Phe Lys Tyr Leu Val Cys Asn Ile Lys Asp Thr Ile  381 965 975 975  383 Phe Gly Glu Glu His Tyr Pro Asp Phe Phe Leu Ser Thr Leu Lys His		Met	Gln	-	Δla	Lvs	Glu	Tvr	-	Asn	Hic	Phe	Lvs	-	Asn	Len	Ala
377 Met Ser Ser Met Ile Asp Leu Glu Val Ser Lys Ile Ile Tyr Ser Val 378 945		1100		0,10		-10		-	~10	P			_	-10			
378       945       950       955       960         380       Thr Arg Ala Phe Phe Lys Tyr Leu Val Cys Asn Ile Lys Asp Thr Ile         381       965       970       975         383       Phe Gly Glu Glu His Tyr Pro Asp Phe Phe Leu Ser Thr Leu Lys His		Met		Ser	Met	Ile	Asp		Glu	Va 1	Ser	Lvs		Tle	Tvr	Ser	Va 1
Thr Arg Ala Phe Phe Lys Tyr Leu Val Cys Asn Ile Lys Asp Thr Ile 381 965 970 975 988 Phe Gly Glu Glu His Tyr Pro Asp Phe Phe Leu Ser Thr Leu Lys His							_	Lou	JIU	,	J C L	_			- 1 -	501	
965 970 975  Phe Gly Glu Glu His Tyr Pro Asp Phe Phe Leu Ser Thr Leu Lys His				Δla	Phe	Phe		Tur	T.eu	Va 1	Cve		T1e	Lve	Asp	Thr	
383 Phe Gly Glu Glu His Tyr Pro Asp Phe Phe Leu Ser Thr Leu Lys His			9		1 110		~y5	-1-	LCu	, 41		11011	110	273			
			Glv	Glu	Glu		Tvr	Pro	Asp	Phe		Len	Ser	Thr			His
JU# CBK 49U 99U	384		1		980		-1-			985			~,~-		990	-, -	

## VERIFICATION SUMMARY DATE: 02/06/2002 PATENT APPLICATION: US/10/054,295 TIME: 15:49:17

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L:32 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:33 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:194 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=2
L:474 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=4
L:591 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=5
L:710 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=6
L:827 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=7
L:974 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=8
L:1151 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=9
L:1180 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=10
L:1213 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=11
L:1243 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=12
L:1275 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=13
L:1302 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=14
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L:1458 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=20
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L:1506 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=22
L:1529 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=23
L:1550 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=24
L:1571 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=25
L:1592 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=26
L:1613 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=27
L:2331 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=54
L:2508 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=55
L:2718 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=58
L:2739 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=59
L:3282 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 68
L:3410 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 68
L:3506 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 68
L:3772 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=70
L:3800 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:71
L:3811 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=72
L:3838 \text{ M}:341 \text{ W}: (46) \text{ "n" or "Xaa" used, for SEQ ID$#:73}
L:3849 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=74
L:3877 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:75
L:3888 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=76
L:3921 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=78
L:4385 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=87
L:4400 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=88
L:4415 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=89
L:4431 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=90
L:4446 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=91
L:4462 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=92
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VERIFICATION SUMMARY
PATENT APPLICATION: US/10/054,295

DATE: 02/06/2002
TIME: 15:49:17

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L:4478 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=93
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L:4510 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=95
L:4526 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=96
L:4542 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=97
L:4558 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=98
L:4574 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=99
L:4717 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:101
L:4815 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=102
L:4831 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=103
L:4846 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=104
L:6621 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:174
L:6624 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:174
L:6627 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:174
L:6630 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:174
L:6639 \text{ M}:341 \text{ W}: \text{ (46) "n" or "Xaa" used, for SEQ ID$$\#:174$}
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L:6645 \text{ M}:341 \text{ W}: (46) \text{ "n" or "Xaa" used, for SEQ ID$#:174}
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L:6706 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:176
L:6725 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:177
L:6728 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:177
L:6924 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:185
L:7297 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:202
L:7300 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:202
L:7303 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:202
L:7315 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:202
L:7318 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:202
L:7324 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:202
L:7365~M:341~W: (46) "n" or "Xaa" used, for SEQ ID#:203
L:7368 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:203
L:7490 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:206
L:7743 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:215
L:7746 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:215
L:7763 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:216 L:7766 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:216
L:7791 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:217
L:7794 \text{ M}:341 \text{ W}: (46) \text{ "n" or "Xaa" used, for SEQ ID$#:217}
L:7797 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:217
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L:7827 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:217
L:7830 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:217 L:7833 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:217
L:7908 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:217
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